

WHAT IS CLAIMED IS:

1. A set of nucleic acids comprising:
 - a first pair of primers, each containing an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and
 - a second pair of primers, each containing an oligo-nucleotide selected from the hexon gene region of adenovirus,wherein each oligo-nucleotide has 14-40 nucleotides in length.
2. The set of nucleic acids of claim 1, further comprising:
 - a third pair of primers, each containing an oligo-nucleotide specific for human parainfluenza virus 1;
 - a fourth pair of primers, each containing an oligo-nucleotide specific for human parainfluenza virus 3;
 - a fifth pair of primers, each containing an oligo-nucleotide specific for respiratory syncytial virus;
 - a sixth pair of primers, each containing an oligo-nucleotide specific for influenza virus A; or
 - a seventh pair of primers, each containing an oligo-nucleotide specific for influenza virus B;
 - or a combination thereof.
3. The set of nucleic acids of claim 2, wherein
 - the oligo-nucleotides in the third pair of primers are selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,
 - the oligo-nucleotides in the fourth pair of primers are selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,
 - the oligo-nucleotides in the fifth pair of primers are selected from the non-structural protein 2 gene region of respiratory syncytial virus,
 - the oligo-nucleotides in the sixth pair of primers are selected from the non-structural protein gene region of influenza virus A, and

the oligo-nucleotides in the seventh pair of primers are selected from the hemagglutinin-neuraminidase gene region of influenza virus B.

4. The set of nucleic acids of claim 1, wherein

the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7; and

the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.

5. The set of nucleic acids of claim 4, further comprising:

a third pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;

a fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ ID NOs:9 and 11;

a fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;

a sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:16 and 18, or SEQ ID NOs:17 and 19; or

a seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID NO:20 and 22, or SEQ ID NOs:21 and 23,

or a combination thereof.

6. A set of nucleic acids comprising:

a first nucleic acid obtained from amplification of a respiratory syncytial virus nucleic acid template with a first pair of primers, each containing an oligo-nucleotide selected from the non-structural protein 2 gene region;

a second nucleic acid obtained from amplification of an influenza virus A nucleic acid template with a second pair of primers, each containing an oligo-nucleotide selected from the non-structural protein gene region; or

a third nucleic acid obtained from amplification of an influenza virus B nucleic acid template with a third pair of primers, each containing an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region,
or a combination thereof,
wherein each oligo-nucleotide has 14-40 nucleotides in length.

7. The set of nucleic acids of claim 6, wherein
the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;
the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs:16 and 18, or SEQ ID NOs:17 and 19; and
the oligo-nucleotides in the third pair of primers are, respectively, SEQ ID NOs:20 and 22, or SEQ ID NOs:21 and 23.
8. The set of nucleic acids of claim 7, further comprising:
a fourth nucleic acid obtained from amplification of a human parainfluenza virus 1 nucleic acid template with a fourth pair of primers, said fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;
a fifth nucleic acid obtained from amplification of a human parainfluenza virus 2 nucleic acid template with a fifth pair of primers, said fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7;
a sixth nucleic acid obtained from amplification of a human parainfluenza virus 3 nucleic acid template with a sixth pair of primers, said sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ ID NOs:9 and 11; or
a seventh nucleic acid obtained from amplification of an adenovirus nucleic acid template with a seventh pair of primers, said seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27;
or a combination thereof.

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- 1 9. A set of nucleic acids comprising:
2 a first nucleic acid containing a first oligo-nucleotide selected from the non-
3 structural protein 2 gene region of respiratory syncytial virus,
4 a second nucleic acid containing a second oligo-nucleotide selected from the non-
5 structural protein gene region of influenza virus A, or
6 a third nucleic acid containing a third oligo-nucleotide selected from the
7 hemagglutinin-neuraminidase gene region of influenza virus B,
8 or a combination thereof,
9 wherein each nucleic acid has 20-1,000 nucleotides in length.

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16. The set of nucleic acids of claim 15, wherein each nucleic acid has 20-500 nucleotides in length.

17. The set of nucleic acids of claim 16, wherein each nucleic acid has 20-50 nucleotides in length.

18. A method of simultaneously detecting viruses which cause respiratory infections comprising:

providing a nucleic acid from a sample suspected of containing a virus to be detected;

amplifying the nucleic acid with a set of primers specific for a group of target viruses, said set of primers containing a first pair of primers, each having an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and a second pair of primers, each having an oligo-nucleotide selected from the hexon gene region of adenovirus, each oligo-nucleotide having 14-40 nucleotides in length; and

detecting amplification products;
whereby detection of an amplification product specific for a target virus indicates the presence of the target virus.

19. The method of claim 18, wherein, in the amplifying step, said set of primers further containing:

a third pair of primers, each including an oligo-nucleotide specific for human parainfluenza virus 1,

a fourth pair of primers, each including an oligo-nucleotide specific for human parainfluenza virus 3,

a fifth pair of primers, each including an oligo-nucleotide specific for respiratory syncytial virus,

a sixth pair of primers, each including an oligo-nucleotide specific for influenza virus A, or

a seventh pair of primers, each including an oligo-nucleotide specific for
influenza virus B,
or a combination thereof.

20. The method of claim 19, wherein
the oligo-nucleotides in the third pair of primers are selected from the
hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,
the oligo-nucleotides in the fourth pair of primers are selected from the
hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,
the oligo-nucleotides in the fifth pair of primers are selected from the non-
structural protein 2 gene region of respiratory syncytial virus,
the oligo-nucleotides in the sixth pair of primers are selected from the non-
structural protein gene region of influenza virus A, and
the oligo-nucleotides in the seventh pair of primers are selected from the
hemagglutinin-neuraminidase gene region of influenza virus B.

21. The method of claim 18, wherein
the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5
and 7, or SEQ ID NOs:6 and 7; and
the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID
NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.

22. The method of claim 21, wherein said set of primers further containing:
a third pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:1
and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;
a fourth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:8
and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;
a fifth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:12
and 14, or SEQ ID NOs:13 and 15;
a sixth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs: 16
and 18, or SEQ ID NOs:17 and 19; or

a seventh pair of primers including, respectively, oligo-nucleotides SEQ ID NO:20 and 22, or SEQ ID NOs:21 and 23;
or a combination thereof.

23. The method of claim 18, wherein the detecting step includes hybridizing the amplification product to a set of probes, said set of probes containing:
 - a first probe having a first nucleic acid selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and
 - a second probe having a second nucleic acid selected from the hexon gene region of adenovirus,each probe having 20-2000 nucleotides in length.
24. The method of claim 23, wherein each nucleic acid is selected from the group consisting of SEQ ID NOs:34-36 and 53-57.
25. The method of claim 19, wherein the detecting step includes hybridizing the amplification product to a set of primers, said set of probes contains:
 - a first probe having a first nucleic acid selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and
 - a second probe having a second nucleic acid selected from the hexon gene region of adenovirus;said set of probes further contains:
 - a third probe having a third nucleic acid specific for human parainfluenza virus 1,
 - a fourth probe having a fourth nucleic acid specific for human parainfluenza virus 3,
 - a fifth probe having a fifth nucleic acid specific for respiratory syncytial virus,
 - a sixth probe having a sixth nucleic acid specific for influenza virus A, or
 - a seventh probe having a seventh nucleic acid specific for influenza virus B,or a combination thereof;
each probe having 20-2000 nucleotides in length.

- 1 26. The method of claim 25, wherein each probe is selected from the group consisting of
2 SEQ ID NOs:28-57.

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